how the inoculant was prepared.

In the next study in 1963 three clinical isolates were tested and one shellfish isolate was tested. It was determined that disease was -- disease developed in one of the strains only. When they went back they found that this was actually Kanagawa positive.

There wasn't really a dose response in this particular experiment that they were looking at. They just gave one dose and four-out-of-four had diarrhea, and I guess usually if you've got diarrhea you've got some abdominal pain that usually comes along with that.

In this particular study the cultures were suspended in milk and then followed by a normal meal.

In the third study Sakazaki, a volunteer study with fifteen Kanagawa negative strains, fourteen of which were from sea fish and one was a non-hemolytic mutant from a Kanagawa positive mutant. I'm not sure exactly the total number, but with doses up as high as ten-to-the-ninth, no disease was observed.

So here again it brings us back to this concept that we've been talking a lot about today that the KP negative strains do not appear to be that pathogenic.

However, there is one report, and this was back in 1971, that disease did occur following the feeding of a

non-hemolytic isolate. This actually wasn't a full report of itself, this is actually a personal communication to this author from the previous author. So there's just a section in there of a personal communication from Sakazaki.

In this particular report, volunteer experiments, it was observed that six to eight hours after feeding a KP positive strain diarrhea resulted.

Eighteen hours after feeding a KP negative strain diarrhea also resulted. In both cases his comment is that the dose was approximately ten-to-the six.

To readdress this idea of KP negative strains, Sanyal in 1974 again looked at three KP negative strains, but this time, instead of environmental isolates that had been utilized in the previous experiments, these were three strains that were obtained from clinical cases. This was also a clinical case, but again, this was a KP positive.

So in here again with these strains, with doses as high as ten-to-the-ten, no disease was observed in these studies.

In contrast to that, one KP positive strain was fed at a dose 200 cells, zero out of four showed any response. When you got up to doses of ten-to-the-five, no

real diarrhea, but there were complaints of abdominal discomfort, and then when up to ten-to-the-seventh, two out of four had diarrhea and two out of four had abdominal.

So, infecting dose, taking these studies, appears to be somewhere between ten-to-the-five and ten-to-the-seven viable cells.

However, there are a lot of uncertainties that must be pointed out when dealing with human feeding trials. Although, as I just suggested, that doses within ten-to-the-five and ten-to-the-six may result in disease, these are studies with very select populations. For the most part you're talking about very healthy study people that are volunteering. So we don't have those possibly susceptible groups that perhaps we've been talking about today already.

In most cases these studies are done with gastric acid neutralization. So they're either given bicarb to neutralize stomach acidity or given in milk to perhaps neutralize stomach acidity, but what effect does that have? Essentially you're setting up that person because you want that person to get sick, so you're setting up the intestinal tract.

Finally, this food matrix effect, what -- are

you presenting those bacteria into the gut? How is that effecting? So you've got a very -- it's a very select and it's a very controlled experiment when you do that.

You also have very many uncertainties when it comes to the pathogen. In those previous studies there, as you know, the date of the last one was 1974, so what was the characterization of that strain? The papers don't talk very much about where — the details of those strains. What is the virulence potential of those particular strains? What was the effect of the growth conditions on virulence? How were those particular cells grown, and what effect did that have on the results that were obtained?

So you do have results from human feeding trials. They give you ranges, but again you have to keep those uncertainties in mind and the model is going to have to account for that.

So what can we do? What's the future of doing additional vibrio parahaemolyticus feeding trials?

For our purposes it would be nice to be able -the most direct approach would be if we were able to spike
oysters with the new outbreak strains that have been
isolated out there, and take those directly to humans.
That may be the most direct answer to some of the

questions that we may have.

Unfortunately, this is unlikely to be repeated this time. And certainly not by July that this is going to occur.

There have been reports, and we talked a little about that earlier, there are reports of sudden death that's been associated with infection with vibrio parahaemolyticus. This is not going to get you through any human use committees. So the prospects of doing this are not likely at all.

It comes to -- in addition, the thermostable direct hemolysin has also been reported to have some cardio toxicity. This is where they feel that there is an issue involved.

So we're not going to be able to do these and repeat what's been done in the past with some of these strains that we'd like to really work with these days.

Where does that leave us? The remaining model that's available are surrogate models. In the absence of additional human data for any particular pathogenic strain or serotype of vibrio parahaemolyticus, the alternate for dose-response modeling is to select an appropriate surrogate bacterial pathogen for which additional dose-response data is either available or can be generated in a

short amount of time.

Additional information that could be considered would be a low dose extrapolation, perhaps looking at some bio-markers. The role of food matrix on infectivity, and also which strain do you pick.

Obviously, the most relevant model would be that of using feedings of human volunteers. But, that may not be again possible. So the other option is what animal models could be used that we could extrapolate information from.

Animal models using vibrio parahaemolyticus or a surrogate organism could be used to provide a basis for extrapolating dose-response estimates for humans. Animal models can be used to assess the virulence potential of different strains and serotypes, to study the role of the specific determinate. As I mentioned before, the effect of food matrixes and other environmental factors on virulence could be used to study dose-response relationships.

All of this could be done much more readily and much more cheaper (sic) in animals.

We may be able to compare VP animal models with other animal models for surrogate pathogens which have feeding, human feeding trial data associated with it.

Then trying to tie those into it. We can correlate animal models together and that second animal model can correlate back to a human feeding trial, then maybe we can gather some additional information on dose response.

In terms of selecting a surrogate there are several criteria that would be looked at.

The first one, taxonomic similarity. It would be nice if the bugs were very closely related, that helps. When you're going to produce inferences to the bug of interest it's nice to know that the bug that you've got is somewhat close.

Also, the mechanism or the genetics of the pathogens in terms of their virulence factors, you'd want those to be close. We've talked in the past, Chuck has brought up pathogenicity islands, toxin genes. So you'd like that to be as close as possible.

Mechanisms of pathogenicity. Is it an invasive organism? Is it a toxin-mediated organism? Again, you would like to have that as closely as you could.

Modes of transmission. The same thing. Is the epidemiology of the organism similar to what we're interested in?

So these again are obviously factors we want to look to, and we would also want quantitative data for dose

and response should exist for these other surrogates. You want information to be available from them.

The next slide gives examples of three surrogate human feeding studies that could be used to model vibrio parahaemolyticus dose-response relationships. They are listed on these slides: vibrio cholera non-01, vibrio cholera 0139 Bengal, and campylobacter jejuni. They include two within the same family, obviously those two, and one that used to be in the same family, campylobacter jejuni that now has moved on to its own family.

This slide describes the two studies with the two cholera strains. Both of these done by Glen Morris, I believe, up in Maryland.

The first one, in 1990, describes studies with vibrio cholera non-01. This is a serotype associated with gastroenteritis, but does not produce the classical cholera enterotoxin. It's been reported to elaborate a toxin that's related to the V.P. hemolysin. It's ubiquitous in estrin environments, and is commonly isolated from shellfish, including oysters.

In this study they had 23 men, 4 women, ages 18 to 34, all of them were pre-treated with sodium bicarbonate. In this study three clinical strains were tested and one out of those three produced disease in

these volunteers.

You will see that the doses are ten-to-the-five, zero with diarrhea, ten-to-the-six, begin seeing two out of three, ten-to-the-seventh, one out of two. You begin seeing disease in the range that was similar to what was seen with the vibrio parahaemolyticus feeding studies.

These were all pre-treated with sodium bicarb before they were given the bacteria.

In the second study, again with Morris, vibrio cholera 0139 is more of a classical cholera. It does produce cholera toxin. It has all the same virulence—associated genes, including the toxar (phonetic) regulon (phonetic) the virulence cassette, all the CTX, Ace, Zot (phonetic), all the different ones that they've got. But, it just doesn't have the genes that have the biosynthesis of the 01 antigen.

Again, in this study volunteers were pre-treated with sodium bicarbonate to neutralize stomach acidity and actually took nothing for 90 minutes before or after the challenge. So in this case you've actually got them challenged on an empty stomach. That's, I think, to make sure that they take all that they're supposed to take.

In this study again at a dose of ten-to-thefour, you have two out of four showing signs of disease.

At a dose of ten-to-the-six you have seven out of nine. Here slightly lower doses than what we saw with vibrio parahaemolyticus. And again noting that this non-01 probably is much more similar in pathogenicity to vibrio parahaemolyticus than this 0139. But, again here's one of the options that's there.

This one just shows the last one, campylobacter jejuni, and as I said, this is a closely related -- was within the family of vibrio at one time and now is closely related.

In this study two strains of campylobacter jejuni ingested by 111 adult volunteers in doses ranging from eight times ten to the two, to two times ten to the ninth were tested. You do see that rates increase with dose, but development of illness did not show a real clear-cut dose response.

Again this brings back this idea of human feeding studies are very -- they are controlled, but you're dealing not with a uniform population, so variability does come into play.

Also in this study with campylobacter jejuni they also fasted for 90 minutes and the challenge was given either in dry milk or they were treated with sodium bicarbonate.

I'd like to now turn to what's out there in terms of animal models for vibrio parahaemolyticus that could be used to extrapolate information on dose-response relationships.

Models that have been described include monkeys, dogs, rabbits, and mice. Some of these models have doseresponse relationship information. Some of these models just deal with virulence potential. So different models we may get different information from them.

The first one was that using monkeys. This came out of the same study of the first feeding study that I described in 1963. Animals were fed the same lots that were actually given to those human volunteers.

In one of three clinical isolates diarrhea was produced along with vomiting at a dose of ten-to-the-tenth. This was the same strain that produced diarrhea in the human feeding trials. So two other strains within that trial did not produce any disease in humans, and they also did not produce any disease in these animals.

No disease was found with one shellfish isolate that was looked at. No real dose-response information, just a model that says, yeah, you can determine virulence using monkeys.

Also as part of the same study oral challenge of

dogs. In this case no disease was found with five of the clinical isolates that were used. Again, going back to that same human feeding trial. One of two shellfish isolates produced diarrhea at a dose of ten-to-the-tenth. So here you have a model that does allow disease, but less discriminatory in terms of what strains you're seeing disease in.

Rabbits have been used for virulence for vibrio parahaemolyticus, and several different rabbit models have been reported.

The first one is described as the oral challenge of infant rabbits. In this study one KP positive strain - well, let me go back.

In this particular study the animals were orally challenged and then seven hours after challenge they were sacrificed and they looked for -- bacteremia was assayed and then liver and spleen cultures were done on all animals.

The results, one KP positive isolate was positive for bacteremia liver and spleen invasion, and one KP negative isolate was negative for bacteremia liver and spleen invasion.

In this case doses again were in the ten-to-theninth, the ten-to-the-tenth range.

It's interesting to note, and we will actually get back to it a little bit later, that the percentage of positive blood cultures was increased when these particular strains were first passed through animals, gotten out of the animal, and then reintroduced into new animals. The extent of bacterium disease actually increased.

This slide shows two other models that have been used with rabbits. The first one is the rabbit ileal loop model and this is something that Chuck alluded to earlier today. This is a in-vivo model, but very set up for infection.

In this particular model essentially you anesthetize animals, surgically open them up, remove their intestinal tract, and tie off a series of blind loops within the intestinal tract.

You then inject samples into these loops, either live bugs, toxin fractions, whatever you want to test, into these loops. Put the loops back into the animal. Sew up the animal. Have the animal survive another 18 to 24 hours. At that time sacrifice, reopen up those, and you look for fluid accumulation within those loops.

Essentially what you come up with is you come up with a ratio of the amount of fluid per centimeter of

tissue length of the loop and that gives you a relative idea of how much fluid is coming into those loops. These have been extensively used for enteric toxins.

The results of these studies have shown that most of the KP positives are positive within this assay and in a study of -- let's see, they used three KP positive strains for this particular study. They had LD 50 ranges, which they described as the dose where 50 percent of the loops were positive. They had as low as ten-to-the-five cells per loop produced positive. They estimated that positive loops were initiated with doses as low as ten-to-the-two cells per loop.

As Chuck mentioned and as the literature does stand firm on, most KP negative strains are generally negative within this assay system.

Recently there have been studies with genetically manipulated strains where the TDH genes have been genetically removed, and in this case the mutants are also negative in the assay where the parent was positive, with the ileal loop assay.

This final one is an in-vitro assay that's out there, it's called using chambers. This is an in-vitro test system. This is a system in which rabbit ileal loop tissue is mounted in chambers, little chambers, and you

add your sample to one side of this chamber. You look for changes in short circuit current that goes through your tissue segment. So you're looking for the ability of your organism or your toxin or whatever to disrupt the integrity of that tissue that you've lined in the wall.

This showed positive response in TDH positive isolates only and a negative response with this particular mutant in the same study, and they've also showed positive responses with purified TDH.

Finally, we'll just talk about some mice models that are out there that have given some dose-response relationship information.

The models that have been reported, IP challenge of adult mice, orogastric challenge of adult mice, and orogastric challenge of infant mice.

The next slide describes those studies with IP challenges. These are composite groups where four TDH clinical strains were used. Three TDH negative clinical strains and five TDH negative food strains were used and inoculated in a dose-response fashion.

You'll see that within these groups mortality was concomitant with the inoculum size. Death rate appeared to be irrespective of the TDH phenotype in inoculum strains. Mice tolerated the lower doses of ten-

to-the-five and ten-to-the six, but administration of doses more than ten-to-the-seventh resulted in sudden increase in the death rate, and by ten-to-the-eight almost all animals were killed upon challenge.

LD 50 dose ranges went from about ten-to-thesixth to ten-to-the-seventh, but no statistical differences were seen between mortalities among the challenged groups. So here's a model where you don't see differences between the TDH negative and the TDH positive.

This is a continuation of the same study, but here the challenges were oral. Again a composite of strains, two TDH positive clinical strains, two TDH negative strains. One was a food. One was a clinical.

Again, you have doses ten-to-the-seventh, ten-to-the-eight, ten-to-the-ninth, and again as before, you're looking at the number of deaths that occurred.

As before, no significant differences were noticed between the challenges dependant on the TDH phenotype.

Mortality rates reached about 80 percent by tento-the-ninth, and they do show a dose-response relationship.

Finally, the last study, just to point out one other model that's available, is the oral challenge of

infant mice. In this study one TDH positive clinical strain was isolated and a dose of ten-to-the-seventh showed a positive fluid accumulation within this animal assay.

This is just an example that was provided by John Bowers, who is the modeler in the group. This illustrates one possible modeling approach using the orogastric and the intraperitoneal challenge data that was just presented with the mice. This is called a Probit or Probit Regression Model.

This model assume that there exists a distribution of sensitivity to the bacteriological agent over the population. I believe more of a normal distribution. It looks at the probability of response. A zero Probit turns out to be -- is the indication of a fifty percent probability of illness. If you move over here you can come up with a LD 50 or an infectious dose.

This is just presented as one option that may be available. That some of the animal model can be used to generate data that does have dose-response relationship information.

Other statistical models will be evaluated, because this model particularly, I guess, is -- well, differences will be different in different models,

depending on if you're looking at the LD 50 or you're looking at low extrapolation doses. So this is just to present that models are out there that can be used, and the data can be incorporated into some of these models.

I'd like to turn now to surrogate animal models.

Again, with the possibility that these may be able to provide some sort of information that we can use.

The first model is going back again to a rabbit model. This is called the removable intestinal tie adult rabbit diarrhea model. For those who are familiar with this and have done a lot of this, I'm not exactly sure who the RITARD is. When you're finished with 30 or so of these you really feel like you've done quite a job.

This was done with the same non-01 vibrio cholera strains that were done with the humans, that Glen Morris reported.

This is also a surgical model. You open up the rabbits, tie off the cecum, put in a little slip knot to put in sort of a blind pouch. You tie off the intestinal tract. Inject the bacteria, sew up the animal, except for this little slip knot. Let that incubate for four hours. Pull the slip knot and then close up the animal. Again, you're setting up the animal for infection.

In this study the severity and extent of

intestinal damage was dose dependant. The higher doses resulted in more severe disease that developed faster.

Mortality occurred quicker as well in the higher doses. At the ten-to-the-ninth dose all died within 24 hours. At the ten-to-the-fourth dose deaths occurred 24 hours later.

It's interesting to note in this study that rabbits challenged with either of the two strains that did not cause disease in the humans, also did not produce any diarrhea in these rabbits. So the only strain that produced positive results in the rabbit model was the same strain that produced positive results in the human studies.

This lends perhaps mechanistics -- this mechanistic similarity lends validity to the use of these models as surrogates.

Also used infant mice model. Again, using non01 vibrio cholera. Results of this are just using sero
dilutions showed in LD 50 of ten-to-the-seventh and an SF
50, which is what they call a fecal staining. This is the
dose that caused death. This is the dose that just
resulted in fecal staining. So you have diarrhea but not
severe enough to cause death. You see it at a lot lower
value than causing death.

Again, these two are just put up here as possibilities that may be used to gain information on things.

I'd like to go back, in the final segment of this talk, to go back to this disease triangle. I'd like to describe what is known about these factors in terms of vibrio parahaemolyticus. At the same time, hopefully this will be a section where it will raise a lot of the uncertainties that I've just described and that have come up throughout the day.

The first one is looking at the pathogen itself. We've talked a lot about the virulence potential of any particular strain. What is the potential of strains and serotypes? Are they all alike? For the most part it's obvious the thermostable direct hemolysin is a major virulence factor.

But, as we've talked about, there are cases that are out there that are from TDH negative strains. Are they pathogenic? Or is it, as Bill alluded to, it's just that we're not taking them out of the samples. It's just that our methods of detection are not good enough.

There are, as Chuck talked about, certain serotypes that seem to have a predominance of disease.

They talked about the 04, the 01, and certainly we heard a

lot about the 03. So are there serotypes out there that are hotter than other ones and are those the ones we have to worry about? How do we account for those?

Some animal models have shown positive responses with TDH negative isolates. Some of the mice data we showed and then there's some work going on at CFSAN right now with some other mice models and some other strains that indicates that you can see disease with TDH minus strains.

There have been reports of Shiga-like cytotoxin in strains of vibrio parahaemolyticus. What is their role? Enterotoxins have also been. Enteroinvasive. There have been tissue culture studies, there have been rabbit studies that have showed invasion of the wall with vibrio parahaemolyticus. What is the role of this in the disease process?

We may have -- what's been reported for a lot of pathogens currently, is what's the role of in-vivo passage? What's the role of the host actually turning on virulence genes within the host and thereby increasing pathogenicity?

As I mentioned before, in the orally challenged suckling rabbits the percentage of positive blood cultures was increased when strains that had been previously passed

in suckling rabbits were used. There seemed to be some turn-on of virulence when they went through these animals.

What unknown virulence factor may be expressed only within the human intestinal tract or another site of infection that we have no idea that's occurring?

Is there a possibility or a possible role of the oyster in regulating virulence potential? What does the oyster do by itself?

This slide, as an aside, I'd just like to introduce you. We've termed jimi jejuni, and this is a campylobacter jejuni. I just want to point out this an EM picture of campylobacter jejuni in the intestines of an animal. We're still working on it, but we really feel when it turns on its antennae and it turns on its eye genes, that this is what really enhances pathogenicity. So, they're out there, we just have to prove them and try to find them.

In terms of host, are there certain populations more susceptible? Dr. Buchanan has brought that up a lot. There are examples of underlying disease and how do we have to model that?

There are papers that show the production of TDH enhanced by bile acids. So the introduction of bile acids into the growth media and those bile acids that are common

in humans have shown four to sixteen-fold increases in TDH. What role does that play?

Iron limitation also enhances virulence in certain models. These are in the mouse model. I think this was just production.

Also we talked about acid adaptation. Chuck talked a little bit about this, or Andy. It was shown in the same paper that in mice acid adaptation enhances virulence in this particular study. What role do these play in the process?

Food matrix again has an effect. We don't know what that is. Enhanced virulence with the addition of mucin. Can the food effect the acid in your stomach so that you lower the acidity that it's supposed to and then increase? Could the food matrix increase bile secretions and influence virulence?

These are questions that have to be answered.

Finally, the last slide just shows again that there's the uncertainties. Each of the models that were out there and that we discussed. Are there epidemiological approaches? Human trials, animal models, or surrogate models, they all have uncertainties. They all have maybe some pluses, but they also do have negatives, and all of these do have to be taken into

account with any model that's going to be developed. Thank you.

DR. MICHAEL JAHNCKE: Questions from the committee? Bob?

DR. ROBERT BUCHANAN: This one is really off the wall too. Bob Buchanan, FDA. We've heard it mentioned several times during the talk as sort of little side comments that there's a high correlation between raw oyster consumption and beer consumption.

DR. DONALD BURR: I think what is an oyster meal? How much butter did they take and how much bread did they eat. How much beer did they drink, and how much alcohol is there?

DR. ROBERT BUCHANAN: Is there anything associated with the human response to alcohol that would in some way enhance the likelihood that vibrio would get through the stomach and establish itself in the intestinal tract?

DR. DONALD BURR: The model that Glen Morris has developed has looked at some -- was that an alcohol model with mice? They tried sort of spiking mice with alcohol and looking for infectivity. I think it didn't work so well. That was another one that was kind of questionable getting through some of the committees. But, there's not

a lot out there. But, I think, as you said, what are they eating a meal in when they're eating their oysters, what else are they taking down?

DR. MICHAEL JAHNCKE: Other questions? Thank you very much, Dr. Burr.

Our last presenter for this session is Dr.

Marianne Miliotis. She will be doing a summary on what
was presented today.

DR. MARIANNE MILIOTIS: In the next five minutes I will summarize everything that's been said to you since the break this morning.

To summarize, the next three slides are a brief outline of a preliminary model we are considering on how we can integrate all the data that you've heard about today.

This slide is an input/output distribution structure of the pre-harvest/harvest module. As you can see, all the factors, all of the outside circles that -- everything that Chuck mentioned, those are parameter distributions and they are going to serve as our input distributions.

These two circles to your right are the VP levels at the time of harvest. Those two circles are the output distributions of this module and will serve as the

input distribution of a post-module.

Here we've taken all the parameters, time to refrigeration, intervention strategies, characteristics of growth, and those are all our input distributions for the post-harvest module. The output of this is the predicted and observed levels of vibrio parahaemolyticus in the oyster at time of consumption.

These output distributions are going to serve as the input distribution of our final module, which is public health. You can see there are predicted VP levels at time of consumption. All of these will enter into our final module, which is distribution of vibrio parahaemolyticus human illness.

This is the final output and this is our endpoint. It's at this time, on the assumption that all the sub-populations have the same percentage of consumption of raw shellfish. This is where we'll find the difference.

Like other people before us and other risk assessments, we plan to run simulations to develop a model obvious different distributions to serve as the framework to better understand the relationship between vibrio parahaemolyticus illness and all the parameters that have been identified today.

So while providing this framework many necessary assumptions will be made. For example, one is assuming that the different sub-populations will eat the same amount of oysters.

The temperature data. We have some data, very sparse data from studies conducted in the seventies. People have taken seawater and put it -- inoculated them with both parahaemolyticus, KP positive and KP negative and left them for various times and different temperatures to see the difference. We may have to use that kind of data and assume that's what happens in the sea as well.

So in conclusion we hope that this risk assessment will provide a scientific framework for the development of food safety guidance and policy to reduce risk of illness.

Hopefully, what we will be able to take this risk assessment to our risk managers and say, here is the data. Together with the ISSC determine principal factors to be considered when developing criteria for the closure and reopening of harvest waters. Evaluate the preventive strategies and reevaluate the current FDA level of ten thousand CFU per gram.

These are all the members of our task force, our internal FDA task force. I'd like to acknowledge all of

them, the different modules of pre-harvest, the postharvest. Then we have the public health module. Thank you all.

DR. MICHAEL JAHNCKE: Thank you very much. What we'll have now is a committee discussion. We'd like to all the NAC members to the table, and also the presenters, at least for the afternoon session. I'd like to invite all the presenters for today to join us at the table. I think that will make discussions much easier.

There are a couple of questions that we as a committee need to consider also. Keep in mind if you have questions on the document itself, which is under Tab 8 of your book, parameter identification for risk assessment on vibrio parahaemolyticus and raw molluscan shellfish. Also keep in mind the three questions that were initially put to us this morning. What other data do we need? Is the scientific approach sound? Are there any comments and suggestions on that?

We are now open for comments and questions. Dane?

MR. DANE BERNARD: Thank you, Mike. Dane
Bernard. I didn't catch in the summary, and it was
probably there, but as to the last presentation and the
summary, I'm unclear as to how prevalence of those that we

think are pathogenic, TDH positive, Kanagawa positive strains, the relatively low percentage, how that's going to be factored into the risk assessment? The last presentation seemed to indicate that there are some indications that maybe that's not the only vibrio parahaemolyticus that we need to worry about, and I think there's always that concern. But, how is that going to be dealt with in the risk assessment? What assumptions are we going to make there? How are we going to use them?

DR. MICHAEL DINOVI: Mike DiNovi. As long as you can determine some relationship, linear, curve, whatever, between the virulent strains and the non, you can factor that into the portion that I'm putting out, where you'll get a distribution of doses. If you know of a relationship you would just factor and we'd just change the shape of the curve accordingly.

DR. ANDY DEPAOLA: Another possibility is from the retail study we've collected thousands of isolates from four, five hundred samples from retail. We will be testing those for the presence of TDH genes. We should be able to get some estimate as to the range of densities of TDH positive amongst oysters at consumption.

DR. MICHAEL JAHNCKE: Peggy?

DR. MARGUERITE NEILL: I'm wondering if you also

are going to use another subtyping method like PFGE. What I'm thinking about is that there's data from vulnificus, if I remember this correctly, that there's multiple PFGE types in the oyster, but there's generally only one in the patient.

DR. ANDY DEPAOLA: That would be correct with vibrio vulnificus.

DR. MARGUERITE NEILL: Do we have any parallel data or pending studies to answer that question for parahaemolyticus? In other words, subtype the -- divide them up by TDH and then PFGE them.

DR. NICHOLAS DANIELS: During the outbreaks in New York and Texas, and at CDC, we actually did subtype by PFGE, but found that serotyping correlated quite nicely with PFGE. That all the 03:K6's were indistinguishable by PFGE.

I think it is a good discriminator. I'm not sure how that would add to a study. Our policy now is to encourage the states to do PFGE of isolates at the states and then --

DR. MARGUERITE NEILL: (interrupting) Human.

DR. NICHOLAS DANIELS: Clinical, human isolates.

DR. MARGUERITE NEILL: I'm talking about the other way around. I'm talking about in the oysters.

DR. ANDY DEPAOLA: I think the PFGE may be more useful as an epidemiological tool, but I don't see where it's going to be that helpful in risk assessment, other than if we can show that perhaps the 03:K6 is more virulent and has a lower infectious dose. Then in that case it may be useful.

DR. NICHOLAS DANIELS: Yeah. Texas did do PFGE of oyster isolates and showed that those isolates were different by PFGE compared to the clinical isolates.

DR. MARGUERITE NEILL: Not to belabor the point, but the oyster isolates are TDH negative.

DR. NICHOLAS DANIELS: Yes.

DR. ANDY DEPAOLA: What little data is available among the TDH positive isolates there's a lot of variability in molecular fingerprinting techniques. This is from some work that we've done with Steve Gentle (phonetic). A lot of that is from Asia. But none that says that there's one particular PFGE that has a lower infectious dose.

DR. MICHAEL JAHNCKE: Other questions. Please remember to identify yourself when the questions are asked, and even responded to. Bob?

DR. ROBERT BUCHANAN: Bob Buchanan, FDA. First, I'd like to commend the group for an obviously tremendous

amount of work that's been done since we last met at the last Advisory Committee.

Second, I'd like to explore a little bit more in the -- Marianne, in your final statement you indicated that you are going to be done simulation modeling. Have you thought of on what types of distributions you're going to be assuming at the different phases of your evaluation, and in a lack of having what appears to be a tremendous amount of data, you have a very few limited studies, if you must default to a specific distribution to assume how you're going to handle that choice?

DR. MARIANNE MILIOTIS: As I said, this is a very -- this is a preliminary model and we haven't quite got to that stage yet. We're just trying to see how we can integrate all the data that we are picking up. The data we do have is the temperature of the salinity in some of the data from Nick Daniels.

DR. MICHAEL JAHNCKE: I have a question. What is your -- for the data that you do have what are your assumptions or your criteria that you're using to either accept and use that data, or reject that data? Does it vary depending on which part of the assessment you're doing? I'm just asking what your base assumptions and criteria are for accepting published data, or not.

DR. CHARLES KAYSNER: Chuck Kaysner, FDA. There is very limited published. There is quite a bit of unpublished data in my laboratory and Andy DePaola has quite a bit that hasn't been published too. But, basically for pre-harvest module there was a relatively low amount of published data. Most of it -- I think in the late seventies is the last time we saw any.

DR. MICHAEL JAHNCKE: I guess my question is even on the published data what criteria are you using — I mean, not all published data may be useable. My question is what is your basic criteria for accepting published data and using it in your risk assessment or saying that it is not appropriate, or incorrectly done, or however you want to put it, but rejecting it?

DR. MARIANNE MILIOTIS: I think as Chuck said, since this is limited data, we have limited published data, we will take everything we can get, as long as it's pertinent to the risk assessment and it will help in our risk assessment.

DR. ANDY DEPAOLA: In the case of the postharvest there is no published data, so we don't have to worry about throwing out too much.

DR. MICHAEL DINOVI: Yeah, and from my point of view, as I mentioned briefly, things have to validate out.

I can't produce a model that suggests we're eating a million pounds of oysters when there's a hundred million pounds sold.

So at the end I feel my section will need to have definite corroborative data probably from the industry. But that's probably the best source.

DR. MICHAEL JAHNCKE: Bob?

DR. ROBERT BUCHANAN: Bob Buchanan, FDA. To follow that up a little bit further, one of the nice things that was available, for example, with the risk assessment that was done on salmonella in eggs was that the end prediction they could then compare against CDC's data on the yearly outbreak rate.

Do you have anything that you see on the horizon that you can use to validate your estimates, or at least determine whether or not you're going to be in ballpark when you come up with an answer?

DR. MICHAEL DINOVI: Yes. We actually saw one small bit, the data from Florida, suggesting on their rates, and Marianne's data and other epidemiological data you already have -- and CDC data, you have numbers of illnesses. We have -- I mean, you can do arithmetic on approximate total intakes, population-wise. You can certainly gin up a crude number without really using any

of this, but that doesn't really get you anywhere.

The reason to break all this out and build up all the variability and uncertainty is so that you can then go take it apart and see what's important.

One of the things that John Bowers will certainly have to do is sensitivity testing on all this. It may turn out that sections we have very little data on don't effect the outcome anyway. So you don't want to spend time and money on that. So yeah, we will have to do all these things. Certainly at the next meeting John Bowers will be out in front showing you the actual numerical models and how they effect the total.

Again, you go back to the first thing, yes, we will have -- you can't say you're going to make ten million people sick when you only have five thousand cases.

DR. ROBERT BUCHANAN: A couple other points on that. I guess this would be directed towards some of the researchers that were telling us about their future plans. While there's a cutoff date of July 6 that Marianne talked about, if the final risk assessment is going to be completed around November, are any of your future studies going to be completed about that time, that you could actually go back and validate your predictions against the

data that you're achieving? I guess I'm directing that to Andy.

DR. ANDY DEPAOLA: This is Andy. The problem with the cooperation with the states is that some are going to be ready to begin earlier and some are going to begin later. So there will be some data, but it won't be complete. There will be data from Alabama since March and I don't know that any of the other states have started their sampling. We have the data Jan Guch has collected from Alabama over the last year. Some Galveston Bay data that may be a little bias because it was after an outbreak last year. I think the State of Washington has quite a bit of data from the last two years.

So, there should be more available date in November, but I think there will still be a fair amount of uncertainty.

DR. MICHAEL JAHNCKE: Bob?

DR. ROBERT BUCHANAN: Again, Bob Buchanan, FDA.

I'll ask the same question of CDC. Are there any plans
under food net to be examining vibrio data and if so, will
any of it be available about the time that this risk
assessment is completed?

DR. NICHOLAS DANIELS: Currently through food net we're trying to come up with estimates of disease

burden for a variety of pathogens, and vibrio is one of them. So we may have some estimates. Currently Paul Mead is working on that, so we may have that by November.

DR. DONALD BURR: This is Don Burr from the FDA. Certainly it's not going to be finished in time, but the FDA is supporting some work again by Glen Morris, where he's actually taking the surrogate organism, the non-01 vibrio cholera and trying to spike oysters with that, and actually feeding those to humans. Then trying to couple that with animal models, the RITARD model, whatever they come up with, to see if they can do some extrapolations with dose-response. It's not going to be there on time, but there is some of that data that's going to hopefully be generated in the future.

DR. MICHAEL JAHNCKE: Other questions? Bob?

DR. ROBERT BUCHANAN: I was just going to say as a general comment, certainly if you can get that kind of data not long after the risk assessment is finished, and it matches up, it certainly is a very strong statement about the effectiveness of this tool.

DR. MICHAEL JAHNCKE: Other questions, comments?
Morrie?

DR. MORRIS POTTER: Again we have an opportunity for comment from the gallery. Any non-committee members

who would like to present information or opinion are welcome to at this time, or to submit information to the written record until that closes.

Dane, did you have something?

MR. DANE BERNARD: Yes, thank you. Dane
Bernard. There was one other question that bothers me a
little bit, because the disease data that's been collected
shows both wound source and food ingestion source. As you
go through and validate the model I'm assuming we're
focusing solely on ingestion as the vehicle. We're going
to tease out those sources, I would trust.

DR. MARIANNE MILIOTIS: This is Marianne
Miliotis. Yes, we are. We are just focusing on
consumption. We're not looking at wound infections or any
other kind of infection.

MR. DANE BERNARD: So as we go through here and we look at the potential impact of interventions and the benefits and the costs of doing those, we'll be focusing solely on that portion exclusively.

DR. MARIANNE MILIOTIS: On consumption of raw molluscan shellfish, yes.

DR. MORRIS POTTER: Morris Potter here. Dane, the data collected by CDC in collaboration with its partners and other federal agencies and state agencies

through the Gulf Coast Surveillance and Food Net, we will be looking at the distinction of food versus non-food sources.

So, the epidemiologic data that will be collected will serve as a barometer for how well we're -- how well the risk assessment matches observed disease.

Again, FDA is taking this risk assessment very seriously. We would very much appreciate data coming from all sources, and people taking advantage of data that exists in various forms to answer the five questions that were written in the Federal Register announcement.

I see Spencer's hand, Spencer Garrett.

MR. SPENCER GARRETT: I'm Spencer Garrett from the National Marine Fishery Service, one of the sponsoring agencies of NACMIF, and let me say I want to echo Bob Buchanan's job well done to you folks for giving us a day-long presentation on vibrio parahaemolyticus certainly in depth and scope.

In my agency risk assessment, just the phrase risk assessment, is one of the most misunderstood things that we deal with. Remember, we're primarily a fishery management agency. We deal with food safety issues preharvest and we do risk assessments to try to mitigate, if you would, or prevent over fishing. It's kind of like a

little bit different twist. Actually, it's kind of like the opposite twist, if you think about that for a moment or two.

But, risk assessment itself from a public health perspective has a very finite meaning. At least I've been told it has a finite meaning.

Internationally at least, and nationally this committee has put out a publication on risk assessment.

International the CODE X Elementarious Commission is going to be adopting just this year at the commission meeting a document entitled, "The General Principles and Guidelines for the Application of Microbiological Risk Assessment."

For all of you who have perhaps not read that document, and I realize you have a very large risk assessment team here, so some probably have and some perhaps have not, I would urge you to read that, because it does give a general road map that one can follow and then be on very good defensible grounds in terms of the transparency of the process, but also recording all of the assumptions that you make.

Just some general comments I'd like to make myself. One, I also agree with Bob that I think that you have to engage in multi endpoints, not just one endpoint. I think you do have to talk about the sub-populations at

risk, and discriminate that statistical probability against the population perhaps that are not at risk.

As a matter of fact, I think the Federal
Register Document indicates that you're going to do that.
We would hope that you would do that.

Secondly, I'm not sure personally myself about the necessary time. I see there are some data gaps, and there are always data gaps when you do things. I certainly understand that. I'm not certain what's drawing the time line.

Finally, this goes to the consumption model.

There was a paper published, I think we may have helped finance it, by TECHWE (phonetic) in 1985, called the "Social Economical Profiles of Oyster Consumption in the United States."

In that particular paper they stratified the oyster consumption by pounds eaten at home, away from home, seasons, you know, summer, fall, winter spring, race being White, Black, and other. Urbanization being whether the oyster eaters were from an urban setting, a suburban setting, or a non-metro setting. Education levels, just like some of the studies that you quoted, but also per capita income. It might be interesting to get a copy of that study and then bounce that against some of the later

studies that have gone on.

From our agency's perspective obviously we'll be following this very closely. If you would like this study we can formally submit this study that's been published to FDA to have it in your quiver so to speak.

We wish you well. It's going to be a very challenging task, I can assure you. Thank you.

MS. ROBIN DOWNEY: My name is Robin Downey, I'm with the Pacific Coast Shellfish Growers Association. I'm going to make a few very brief comments. I'm actually making them on behalf of the entire shellfish community, with the Molluscan Shellfish Institute, and the Louisiana Oyster Task Force, and the Gulf Oyster Industry Council. We have all been meeting together and talking about this issue for some time.

I'd like to state a few obvious points.

Obviously, we all have been talking about this. There are several studies right now that are being conducted on this issue. It does seem a bit premature to go ahead and try to ramrod this whole process in this risk assessment before all that information is in. I know that there are some political things that are kind of driving this, but I would urge this committee, if at all possible, to hold this off for another year until that information is in.

I'm curious as to why there's been so much information about vulnificus included in the information today. I do urge you to keep vulnificus and parahaemolyticus very much apart from each other.

I'm also concerned that the differences between the different coasts have not really come forward today in the information that's been presented. I would be happy, as a representative of the West Coast to provide information to this committee where you are lacking information.

For example, when the information was provided on harvesting and processes for harvesting, what was presented is not indicative of what we do on the West Coast at all.

Some of the statistics that were provided in this information forum today were somewhat inaccurate.

I've talked to a couple of you about that. I'll be happy to provide that information.

I think the whole shellfish community can say that we'd be happy to provide that information.

Also, there was no differences really noted in commercial versus recreational illnesses. Washington State does have that information. I urge you to please separate those two issues. They are different.

With all that said, I would just like this committee to keep in perspective food-borne illnesses and that shellfish illnesses really constitute a very small percentage of what food-borne illnesses happen in this country.

However, we're happy for the work that's being done here. I think it's very necessary. We certainly want to keep our consumers healthy. I'd like to thank all of you for the work that you will be doing.

DR. MORRIS POTTER: Thank you very much for those comments, and for the offer for information. We would be very anxious to have as much information on industry practices and consumption data as we can get to make the risk assessment that we do as correct and robust as possible.

As far as why now and why not a year from now. A year from now there will also be unanswered questions and more date in the offing. I think once we have a risk assessment framework developed, inserting or replacing data points or distributions in the model becomes a bit easier. I'm not sure that we lose a lot by moving ahead. But, thank you very much for the offer. We will be anxious to see what information you can share.

Dane?

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MR. DANE BERNARD: Thank you. Dane Bernard.

The commenter brings up a couple of good points. I agree with Dr. Potter's comment. To move ahead puts together a framework that allows us to plug in data as it comes along and refine our output.

I think the place to use caution is once we get to a point of having some output of some kind from the risk assessment. Do we have enough confidence in that output to make decisions? I think at that point one should look at what data is in the pipeline, what studies are close enough to then say can we go ahead and make a decision or should we wait on making policy decisions.

I think the point that was made is that there may be some additional data which will allow us to make better policy decisions, and it's at that point that we need to think about the risk management decisions that we make as a result of the output in light of the closeness of additional information.

Also, I think we need to be very clear once we get to the point of having some output as to the degree of confidence we have in the output, the level of uncertainty. One of the problems that I see with certain risk assessments is that while the uncertainties involved in the estimates are in the reports, they're not usually

up-front. You have to dig through the reports. I personally think that we need to be more clear about how accurate our predictions are and what the range of uncertainty is so that once we put out a report it's clear as to what its limitations are.

DR. MORRIS POTTER: Thank you for that counsel, Dane. Cathy?

MS. CATHY DONNELLY: Cathy Donnelly. I'm wondering if the CDC has any plans to do a population-based active surveillance for this pathogen. It seems with the increase in cases over recent years, coupled with the fact that about 88 percent of the cases involve hospitalization, it seems it would be well set up for that type of study.

DR. NICHOLAS DANIELS: We're doing active surveillance in our food net sites, and vibrio is infection that we do have surveillance for. We'll have data from that.

MS. CATHY DONNELLY: Will that also include going back to the patient's home and pulling food samples?

DR. NICHOLAS DANIELS: Usually if there's a culture-positive case in a food net site, that patient is interviewed and it includes sort of a trace-back of where those oysters were harvested, how many that person ate,

how they consumed the oysters. So we do get a lot of information from that. We are asking food net sites to forward isolates to us for subtyping.

DR. MORRIS POTTER: Peggy?

DR. MARGUERITE NEILL: Peggy Neill. I was just going to raise one issue about the food net surveillance particularly for this organism, because as bad as it was for the lack of culturing by so many laboratories for e-coli 0157, I mean, it's in orders of magnitude greater for vibrio. I'm in Rhode Island, which is a coastal state.

Massachusetts, Rhode Island, and Connecticut have probably less than ten percent of the labs that are routinely with culture media on hand for the detection of vibrio.

So therein, I think, lies the real difficulty to look toward food nets for that answer, even though it's in a position to give it, if the supporting labs were doing routinely.

DR. NICHOLAS DANIELS: We did do a laboratory survey in the food net sites and found that around 20 percent of labs routinely use TCBS, but again, that's a small fraction of the labs in food net.

DR. MORRIS POTTER: Other comments? Around the table? Committee away from the table? Others? Guests?

No parting shots?

Thank you all very much. I'd like to thank the Risk Assessment Task Force for doing a very good risk assessment start here, and for making a very nice presentation.

I'd like to thank the committee for its forbearance and all of our guests for joining us today.

(Whereupon, the proceedings in the aboveentitled matter were concluded at 4:10 p.m.)

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I, ANNE I. MAZIORKA, CERT, a Notary Public within and for the County of Cook and State of Illinois, do hereby certify:

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